Enhancing Hit Identification in *Mycobacterium tuberculosis* Drug Discovery Using Dual-Event Bayesian Models

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Table S1. Mean (SD) leave one out and leave out 50% x 100 cross validation of previously published Bayesian models (ROC =receiver operator characteristic) – data from [22]

Dataset (number of molecules)	Leave one out ROC	Leave out 50% x 100 External ROC Score	Leave out 50% x 100Internal ROC Score	Leave out 50% x 100 Concordance	Leave out 50% x 100 Specificity	Leave out 50% x 100 Sensitivity
MLSMR All single point screen (N = 220,463)	0.88	0.86 (0)	0.86 (0)	78.56 (1.86)	78.59(1.94)	77.13 (2.26)
MLSMR dose response set (N = 2273)	0.78	0.73 (0.01)	0.75 (0.01)	66.85 (4.06)	67.21 (7.05)	65.47 (7.96)